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Felicia Walker
(Print Name)

Date: July 27, 2000

Felicia Walker
(Signature)

PATENT APPLICATION **Docket No: 8636**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application

Batch No. 435-188.000
Notice of Allowance Date: 10/6/99

Inventor's Name(s): Gelfand et al.

Art Unit: 1651

Serial No. 07/873,897, filed April 24, 1992

Examiner: D. Naff

For: **PURIFIED THERMOSTABLE ENZYME**

TRANSMITTAL OF FORMAL DRAWINGS

Assistant Commissioner for Patents
Washington, D.C. 20231

Alameda, CA
July 27, 2000

Draftsperson:

The Notice of Draftsperson's Patent Drawing Review attached to Paper 49, mailed July 17, 2000, indicated that Fig. 1-1 to Fig. 1-6 should be labeled Fig. 1A – 1F. Enclosed are the amended formal drawings, Figures 1-A through 1-F, (six sheets) for filing in the above-identified U.S. Patent Application. The amendments are of a purely formal nature and do not introduce new matter. Applicants request entry of the drawings.

Respectfully submitted,

Douglas A. Petry, Ph.D.
Agent for Applicant
(Reg. No. 35,321)
Customer No: **22829**
Telephone: (510) 814-2974
Telefax: (510) 814-2973

10.06.99

TAQ DNA POLYMERASE SEQUENCE FIG.1-A

```
-120                -100                -80
      BglII                          PvuII
AAGCTCAGATCTACCTGCCTGAGGGCGTCCGGTTCCAGCTGGCCCTTCCCGAGGGGGAGA

-60                 -40                 -20
GGGAGGCGTTTCTAAAAGCCCTTCAGGACGCTACCCGGGGGCGGGTGGTGGAAGGGTAAC

1                   20                  40                  60
ATGAGGGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTGGACGGCCAC
MetArgGlyMetLeuProLeuPheGluProLysGlyArgValLeuLeuValAspGlyHis
  1

                    80                  100                 120
CACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCAGCCGGGGGGAGCCG
HisLeuAlaTyrArgThrPheHisAlaLeuLysGlyLeuThrThrSerArgGlyGluPro

                    140                 160                 180
GTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGGCCCTCAAGGAGGACGGGGAC
ValGlnAlaValTyrGlyPheAlaLysSerLeuLeuLysAlaLeuLysGluAspGlyAsp
 41

                    200                 220                 240
GCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCTCCTTCCGCCACGAGGCCTACGGGGGG
AlaValIleValValPheAspAlaLysAlaProSerPheArgHisGluAlaTyrGlyGly

                    260                 280                 300
TACAAGGCGGGCCGGGCCCCCACGCCGGAGGACTTTCCCCGGCAACTCGCCCTCATCAAG
TyrLysAlaGlyArgAlaProThrProGluAspPheProArgGlnLeuAlaLeuIleLys
 81

                    320                 340                 360
                                   XhoI
GAGCTGGTGGACCTCCTGGGGCTGGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGAC
GluLeuValAspLeuLeuGlyLeuAlaArgLeuGluValProGlyTyrGluAlaAspAsp
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-B

```
                    380                 400                 420
GTCCTGGCCAGCCTGGCCAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACC
ValLeuAlaSerLeuAlaLysLysAlaGluLysGluGlyTyrGluValArgIleLeuThr
121

                    440                 460                 480
GCCGACAAAGACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGG
AlaAspLysAspLeuTyrGlnLeuLeuSerAspArgIleHisValLeuHisProGluGly

                    500                 520                 540
Asp718
TACCTCATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGCC
TyrLeuIleThrProAlaTrpLeuTrpGluLysTyrGlyLeuArgProAspGlnTrpAla
161

                    560                 580                 600
GACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGGCATCGGG
AspTyrArgAlaLeuThrGlyAspGluSerAspAsnLeuProGlyValLysGlyIleGly

                    620                 640                 660
                HindIII
GAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAGCCCTCCTCAAGAAC
GluLysThrAlaArgLysLeuLeuGluGluTrpGlySerLeuGluAlaLeuLeuLysAsn
201

                    680                 700                 720
CTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGGCCCACATGGACGATCTGAAG
LeuAspArgLeuLysProAlaIleArgGluLysIleLeuAlaHisMetAspAspLeuLys

                    740                 760                 780
CTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCTGCCCCTGGAGGTGGACTTCGCCAAA
LeuSerTrpAspLeuAlaLysValArgThrAspLeuProLeuGluValAspPheAlaLys
241

                    800                 820                 840
AGGCGGGAGCCCGACCGGGAGAGGCTTAGGGCCTTTCTGGAGAGGCTTGAGTTTGGCAGC
ArgArgGluProAspArgGluArgLeuArgAlaPheLeuGluArgLeuGluPheGlySer
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-C

```
                  860                 880                 900
                                    BstXI
CTCCTCCACGAGTTCGGCCTTCTGGAAAGCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
LeuLeuHisGluPheGlyLeuLeuGluSerProLysAlaLeuGluGluAlaProTrpPro
281                 290

                  920                 940                 960
CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGAT
ProProGluGlyAlaPheValGlyPheValLeuSerArgLysGluProMetTrpAlaAsp

                  980                1000                1020
CTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAA
LeuLeuAlaLeuAlaAlaAlaArgGlyGlyArgValHisArgAlaProGluProTyrLys
321

                 1040                1060                1080
GCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCC
AlaLeuArgAspLeuLysGluAlaArgGlyLeuLeuAlaLysAspLeuSerValLeuAla

                 1100                1120                1140
CTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCTCCTG
LeuArgGluGlyLeuGlyLeuProProGlyAspAspProMetLeuLeuAlaTyrLeuLeu
361

                 1160                1180                1200
GACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGAGTGGACGGAG
AspProSerAsnThrThrProGluGlyValAlaArgArgTyrGlyGlyGluTrpThrGlu

                 1220                1240                1260
GAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTT
GluAlaGlyGluArgAlaAlaLeuSerGluArgLeuPheAlaAsnLeuTrpGlyArgLeu
401

                 1280                1300                1320
GAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTC
GluGlyGluGluArgLeuLeuTrpLeuTyrArgGluValGluArgProLeuSerAlaVal
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-D

```
                1340                1360                1380
CTGGCCCACATGGAGGCCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCC
LeuAlaHisMetGluAlaThrGlyValArgLeuAspValAlaTyrLeuArgAlaLeuSer
441

                1400                1420                1440
                          XhoI
CTGGAGGTGGCCGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCAC
LeuGluValAlaGluGluIleAlaArgLeuGluAlaGluValPheArgLeuAlaGlyHis

                1460                1480                1500
                      PvuII
CCCTTCAACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTT
ProPheAsnLeuAsnSerArgAspGlnLeuGluArgValLeuPheAspGluLeuGlyLeu
481

                1520                1540                1560
CCCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAG
ProAlaIleGlyLysThrGluLysThrGlyLysArgSerThrSerAlaAlaValLeuGlu

                1580                1600                1620
                                    PstI          SacI
GCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAG
AlaLeuArgGluAlaHisProIleValGluLysIleLeuGlnTyrArgGluLeuThrLys
521

                1640                1660                1680
CTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCGCCTC
LeuLysSerThrTyrIleAspProLeuProAspLeuIleHisProArgThrGlyArgLeu

                1700                1720                1740
CACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCGATCCCAAC
HisThrArgPheAsnGlnThrAlaThrAlaThrGlyArgLeuSerSerSerAspProAsn
561

                1760                1780                1800
                                    BamHI
CTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCGGGCCTTCATCGCC
LeuGlnAsnIleProValArgThrProLeuGlyGlnArgIleArgArgAlaPheIleAla
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-E

1820 1840 1860

SacI

GAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGATA*GAGCTC*AGGGTGCTGGCC
GluGluGlyTrpLeuLeuValAlaLeuAspTyrSerGlnIleGluLeuArgValLeuAla
601

1880 1900 1920

CACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACG
HisLeuSerGlyAspGluAsnLeuIleArgValPheGlnGluGlyArgAspIleHisThr

1940 1960 1980

PvuII

GAGACCGC*CAGCTG*GATGTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGG
GluThrAlaSerTrpMetPheGlyValProArgGluAlaValAspProLeuMetArgArg
641

2000 2020 2040

GCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAG
AlaAlaLysThrIleAsnPheGlyValLeuTyrGlyMetSerAlaHisArgLeuSerGln

2060 2080 2100

NheI

GA*GCTAGC*CATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTC
GluLeuAlaIleProTyrGluGluAlaGlnAlaPheIleGluArgTyrPheGlnSerPhe
681

2120 2140 2160

CCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG
ProLysValArgAlaTrpIleGluLysThrLeuGluGluGlyArgArgArgGlyTyrVal

2180 2200 2220

GAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTG
GluThrLeuPheGlyArgArgArgTyrValProAspLeuGluAlaArgValLysSerVal
721

TAQ DNA POLYMERASE SEQUENCE

```
                2240                2260                2280
                .                   .                   .
CGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCGACCTC
ArgGluAlaAlaGluArgMetAlaPheAsnMetProValGlnGlyThrAlaAlaAspLeu
741

                2300                2320                2340
                .                   .                   .
ATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGGCCAGGATGCTC
MetLysLeuAlaMetValLysLeuPheProArgLeuGluGluMetGlyAlaArgMetLeu

                2360                2380                2400
                                 XhoI
                .                   .                   .
CTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGAGGGCGGAGGCCGTGGCC
LeuGlnValHisAspGluLeuValLeuGluAlaProLysGluArgAlaGluAlaValAla
781

                2420                2440                2460
                .                   .                   .
CGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAG
ArgLeuAlaLysGluValMetGluGlyValTyrProLeuAlaValProLeuGluValGlu

                2480                2500
                .                   .
GTGGGGATAGGGGAGGACTGGCTCTCCGCCAAGGAGTGATACCACC
ValGlyIleGlyGluAspTrpLeuSerAlaLysGluEnd
821                                 832
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FIG.1-F